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351 gattgcatat ttttatatat ccaggatgat ggggcatgtg ttctttagaa
401 tctcccaaaa ccatgatata gaatcattg gtaatgacta attattgtgc
451 ttctt

Figure 1. Partial cDNA sequence of Shinc-1 gene.

The partial nucleotide sequence of a Shinc-1 cDNA fragment (456 bp) isolated from human prostate cancer cells (DU-145) by the differential display of mRNA approach is shown.

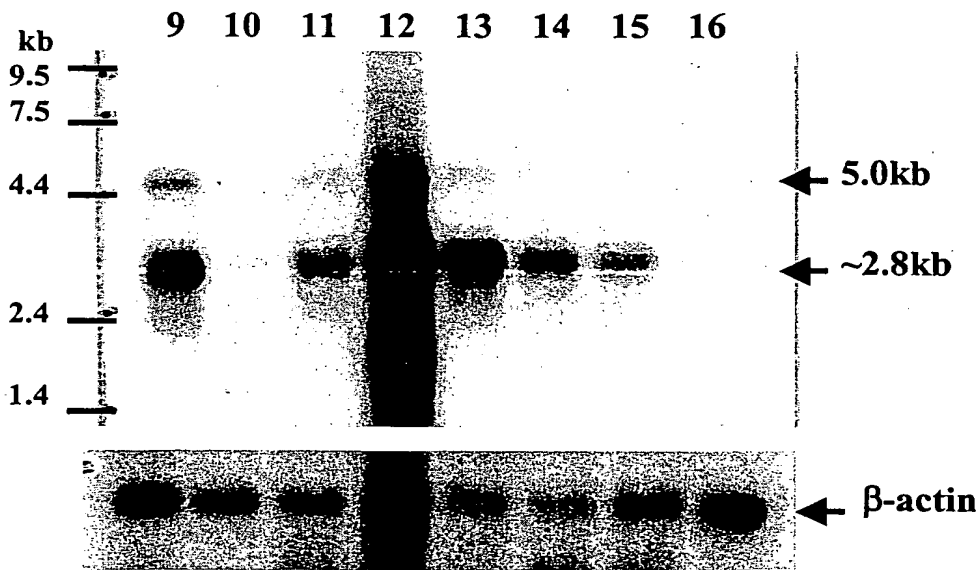
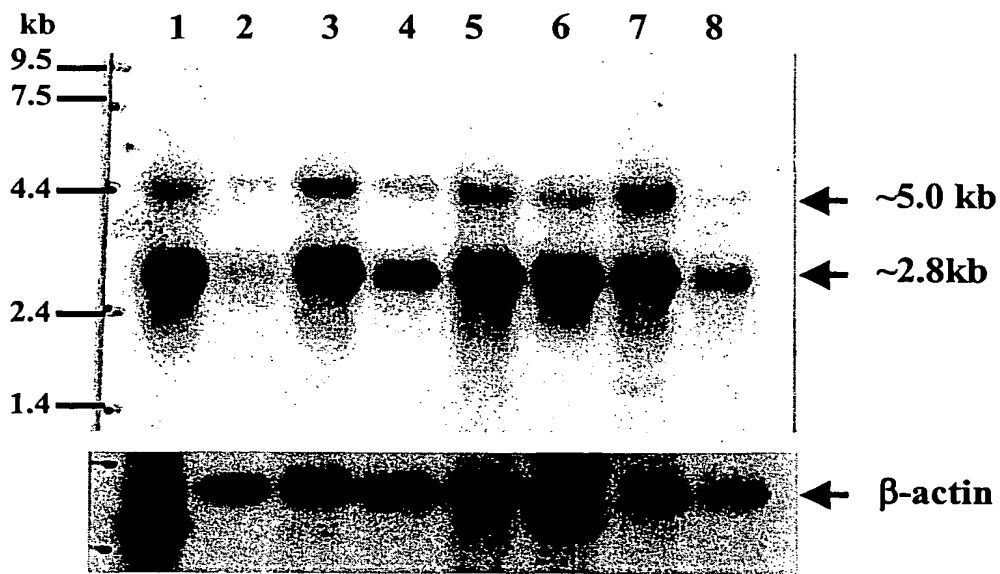


Figure 2. Expression on Shinc-1 mRNA in normal human tissues.

Blots were hybridized with radiolabeled Shinc-1 cDNA probe followed by β -actin cDNA probe.

Lane 1: Heart; lane 2: Brain; lane 3: Placenta; lane 4: Lung; lane 5: Liver; lane 6: Skeltal muscle; lane 7: Kidney; lane 8: Pancreas; lane 9: Spleen; lane 10: Thymus; lane 11: Prostate; lane 12: Testis; lane 13: Ovary; lane 14: Small intestine; lane 15: Colon; lane 16: Peripheral blood leukocytes. Approximately 5.0 kb and 2.8 kB Shinc-1 transcripts are shown.

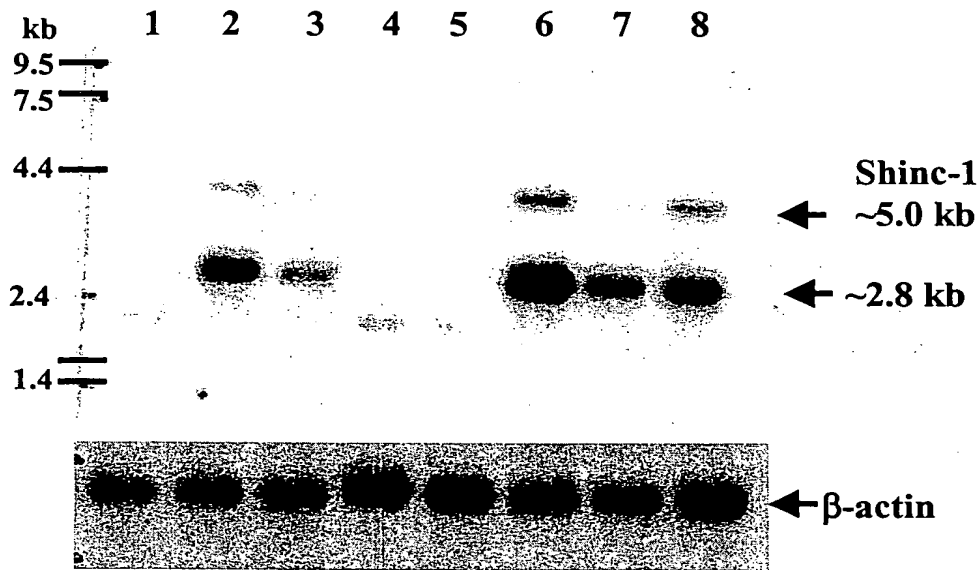
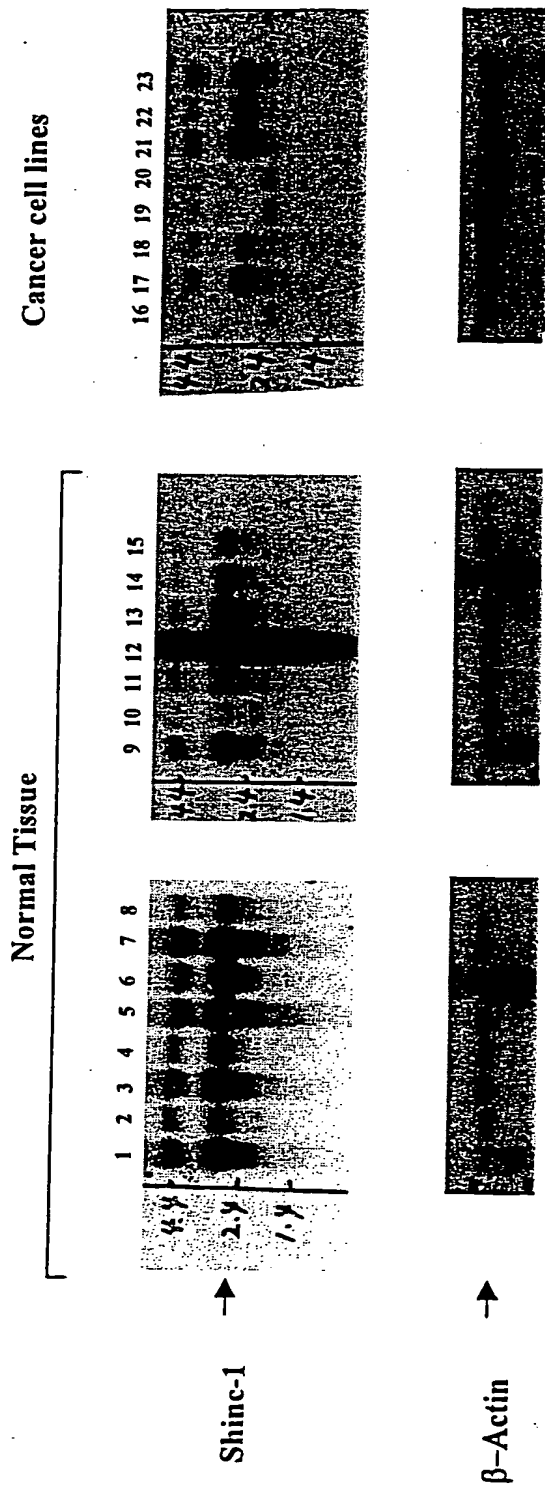


Figure 3. Expression of Shinc-1 mRNA in human cancer cells.

Blots were sequentially probed with radiolabeled Shinc-1 (upper panels) and β -actin (lower panels) cDNA probes. HL-60, promyelocytic leukemia (lane 1); HeLa-S3, (lane 2); K-562, chronic myelogenous leukemia (lane 3); MOLT-4, lymphoblastic leukemia (lane 4); BL-RAJI, Burkitt's lymphoma (lane 5); SW480, colorectal adenocarcinoma (lane 6); A549, lung carcinoma (lane 7); G361, melanoma (lane 8).

FIGURE 4



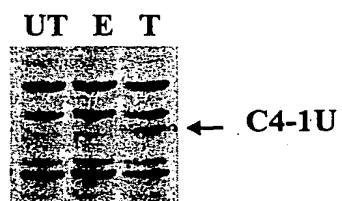


Figure 5. Identification of differentially expressed C4-1U cDNA fragment in DU-145 cells treated with tempo. DU-145 cells were treated for 2 h with 7.5 mM tempo (T), or vehicle (ethanol 1%. E) or left untreated (UT). Total cellular RNA was extracted using RNazol B (Tel-Test Inc, Texas).

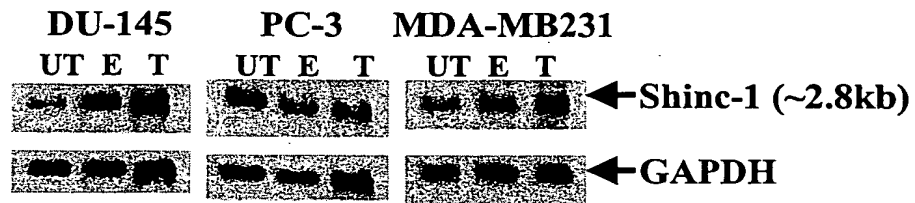


Figure 6. Northern blot hybridization analysis of Shinc-1 gene expression in tempo-treated human prostate (DU-145 and PC-3) and breast cancer cells (MDA-MB 231).

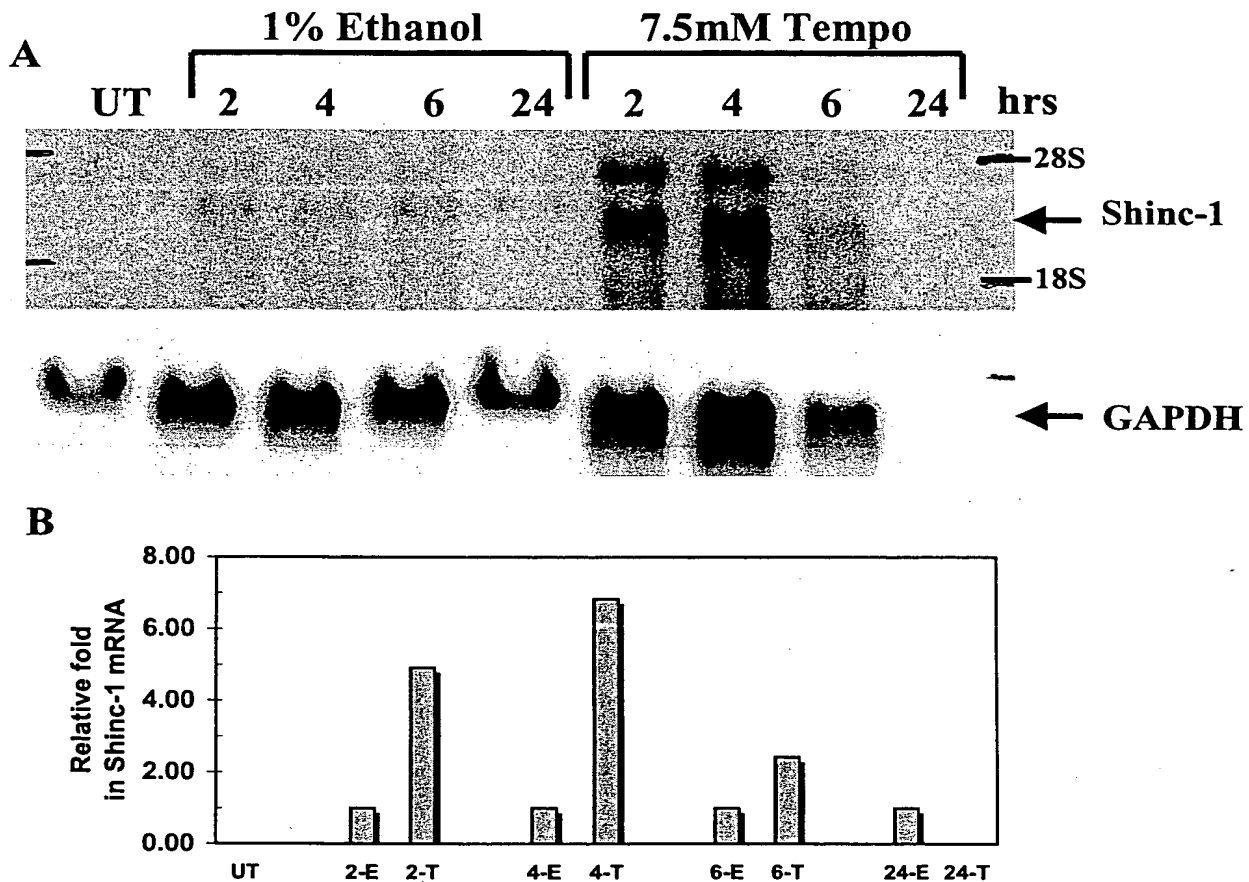


Figure 7. Time-course analysis of Shinc-1 mRNA expression in tempo-treated cells

(A) DU-145 cells were treated with 7.5mM tempo or 1% ethanol for the indicated time. Total RNA were extracted from the cells and fractionated by electrophoresis.

(B) Autoradiographs were computer-scanned using the Image-Quant software (Molecular Dynamics). Relative fold change in the steady-state mRNAs level were calculated by normalizing against the GAPDH signal, followed by comparison with the expression in ethanol-treated and tempo-treated cells. UT: untreated, E: ethanol, T: tempo